EST

Reverse transcriptase domain

Y

1 2   A   B C D   * 3' UT

aa 500

aa 1104

1   α   β   2   3

SH3 domain
binding site

Intron(s)

Exon(s) deleted

Exon(s) inserted
or unspliced intron

Non-coding

Intron(s)

* Stop codon

Fig. 7A

Variants:	1	α	β	2	3
RT-PCR product	NO	+	+	NO	+ & −
PCR from LIM1215 lib.	−	+	−	+	NO
RT-PCR product	NO	−	+	NO	+
53.2 cDNA	−	−	−	−	NO

Fig. 7B

sequence "Y" 104-105 bases
```
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
 AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
  ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla
```

```
CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
 AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
  ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal
```

sequence "1" 38 bases
```
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys
```


sequence "/α" 36 bases
```
GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln
```

sequence "/β" 182 bases
```
GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu
```

```
CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu
```

```
AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis
```

```
GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys
```


partial sequence "2" unknown length
```
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
 Ter
```

```
GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...
```


Fig. 10A